STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/508,759A
Source: IFW16
Date Processed by STIC: 7/27/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**http://www.uspto.gov/ebc/efs/downloads/documents.htm**> , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):** U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/508,759A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1	Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2	Invalid Line Length	The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
3	Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
4	Non-ASCII	The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
5	Variable Length	Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6	PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
7	Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
8	Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence. <210> sequence id number <400> sequence id number 000
9	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
10	Invalid <213> Response	Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)
11	Use of <220>	~~Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses.~~ Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules
12	PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13	Misuse of n/Xaa	"n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid

IFW16

RAW SEQUENCE LISTING DATE: 07/27/2006
PATENT APPLICATION: **US/10/508,759A** TIME: 09:57:33

Input Set : **A:\30215APG_SEQ.txt**
Output Set: **N:\CRF4\07272006\J508759A.raw**

Does Not Comply
Corrected Diskette Needed
see pp 2-5

```
      3 <110> APPLICANT: APROGEN INC.
      5 <120> TITLE OF INVENTION: HUMANIZED ANTIBODY AND PROCESS FOR PREPARING SAME
      7 <130> FILE REFERENCE: PCA30215/APG
C-->  9 <140> CURRENT APPLICATION NUMBER: US/10/508,759A
C-->  9 <141> CURRENT FILING DATE: 2004-09-22
      9 <150> PRIOR APPLICATION NUMBER: KR10-2002-0015708
     10 <151> PRIOR FILING DATE: 2002-03-22
     12 <160> NUMBER OF SEQ ID NOS: 38
     14 <170> SOFTWARE: KopatentIn 1.71
     16 <210> SEQ ID NO: 1
     17 <211> LENGTH: 345
     18 <212> TYPE: DNA
     19 <213> ORGANISM: Artificial Sequence
     21 <220> FEATURE:
     22 <223> OTHER INFORMATION: HEAVY CHAIN of HZVII
     24 <400> SEQUENCE: 1
     25 caggtccagc tggtgcagtc tggagctgaa gtgaagaagc ctggggcctc agtgaaggtt      60
     27 tcctgcaaag cttctggcta caccttcacc agtgcttgga tgaactgggt gcgacaggcc     120
     29 cctggacagg gtcttgagtg gatgggacgg atttatccta gtggtggaag cactagctac     180
     31 gcacagaagt tccagggcag agtcacaatg actgcagaca aatccacgag cacagtctac     240
     33 atggagctca gcagcctgag atctgaggac acggcggtgt attactgtgc aagagagtac     300
     35 cgggttgccc gttggggcca aggaactctg gtcactgtct cttca                     345
     38 <210> SEQ ID NO: 2
     39 <211> LENGTH: 115
     40 <212> TYPE: PRT
     41 <213> ORGANISM: Artificial Sequence
     43 <220> FEATURE:
     44 <223> OTHER INFORMATION: HEAVY CHAIN of HZVII
     47 <400> SEQUENCE: 2
     48 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Ala Pro Gly Ala
     49   1               5                  10                  15
     51 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Ala
     52              20                  25                  30
     54 Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
     55          35                  40                  45
     57 Gly Arg Ile Tyr Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
     58      50                  55                  60
     60 Gln Gly Arg Val Thr Met Thr Ala Asp Lys Ser Thr Ser Thr Val Tyr
     61  65                  70                  75                  80
     63 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
     64                  85                  90                  95
     66 Ala Arg Glu Tyr Arg Val Ala Arg Trp Gly Gln Gly Thr Leu Val Thr
     67              100                 105                 110
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Input Set : **A:\30215APG_SEQ.txt**
Output Set: **N:\CRF4\07272006\J508759A.raw**

69 Val Ser Ala
70 115
73 <210> SEQ ID NO: 3
74 <211> LENGTH: 336
75 <212> TYPE: DNA
76 <213> ORGANISM: Artificial Sequence
78 <220> FEATURE:
79 <223> OTHER INFORMATION: LIGHT CHAIN of HZVII
82 <400> SEQUENCE: 3
83 gatatcgtga tgacccaaac tccactttct ttgtcggtta cccctggaca accagcctct 60
85 atctcttgca agtcaagtca gagcctctta tatagtaatg gaaaaaccta tttgaattgg 120
87 ttattacaga agccaggcca gcctccacag cgcctaatct atctggtgtc taatcgggac 180
89 tctggagtcc ctgacaggtt cagtggcagt ggatcaggaa cagattttac actgaaaatc 240
91 agcagagtgg aggctgagga tgttggagtt tattactgcg tgcaaggtac acattttcct 300
93 cagacgttcg gtggaggcac caaggtggaa atcaaa 336
96 <210> SEQ ID NO: 4
97 <211> LENGTH: 112
98 <212> TYPE: PRT
99 <213> ORGANISM: Artificial Sequence
101 <220> FEATURE:
102 <223> OTHER INFORMATION: LIGHT CHAIN of HZVII
105 <400> SEQUENCE: 4
106 Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
107 1 5 10 15
109 Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser
110 20 25 30
112 Asn Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Lys Pro Gly Gln Pro
113 35 40 45
115 Pro Gln Arg Leu Ile Tyr Leu Val Ser Asn Arg Asp Ser Gly Val Pro
116 50 55 60
118 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
119 65 70 75 80
121 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Val Gln Gly
122 85 90 95
124 Thr His Phe Pro Gln Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
125 100 105 110
130 <210> SEQ ID NO: 5
131 <211> LENGTH: 26
132 <212> TYPE: DNA
133 <213> ORGANISM: Artificial Sequence
135 <220> FEATURE:
136 <223> OTHER INFORMATION: Ryu94
139 <400> SEQUENCE: 5
140 gagaattcac attcacgatg tacttg 26
143 <210> SEQ ID NO: 6
144 <211> LENGTH: 33
145 <212> TYPE: DNA
146 <213> ORGANISM: Artificial Sequence
148 <220> FEATURE:

insufficient - give source of genetic material (see item 11 on Error Summary Sheet)

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Input Set : A:\30215APG_SEQ.txt
Output Set: N:\CRF4\07272006\J508759A.raw

149 <223> OTHER INFORMATION: HUR43-1 same end
152 <400> SEQUENCE: 6
153 ctgctgcagc tggacctgac tctggacacc att 33
156 <210> SEQ ID NO: 7
157 <211> LENGTH: 33
158 <212> TYPE: DNA
159 <213> ORGANISM: Artificial Sequence
161 <220> FEATURE:
162 <223> OTHER INFORMATION: HUR44-1
165 <400> SEQUENCE: 7
166 caggtccagc tgcagcagtc tggacctgaa ctg 33
169 <210> SEQ ID NO: 8
170 <211> LENGTH: 33
171 <212> TYPE: DNA
172 <213> ORGANISM: Artificial Sequence
174 <220> FEATURE:
175 <223> OTHER INFORMATION: HUR45-1
178 <400> SEQUENCE: 8
179 tgggccttg gtggaggctg cagagacagt gac 33
182 <210> SEQ ID NO: 9
183 <211> LENGTH: 33
184 <212> TYPE: DNA
185 <213> ORGANISM: Artificial Sequence
187 <220> FEATURE:
188 <223> OTHER INFORMATION: HUR46-1
191 <400> SEQUENCE: 9
192 gcctccacca agggcccatc ggtcttcccc ctg 33
195 <210> SEQ ID NO: 10
196 <211> LENGTH: 28
197 <212> TYPE: DNA
198 <213> ORGANISM: Artificial Sequence
200 <220> FEATURE:
201 <223> OTHER INFORMATION: HUR31
204 <400> SEQUENCE: 10
205 cagcggccgc tcatttaccc ggggacag 28
208 <210> SEQ ID NO: 11
209 <211> LENGTH: 26
210 <212> TYPE: DNA
211 <213> ORGANISM: Artificial Sequence
213 <220> FEATURE:
214 <223> OTHER INFORMATION: Ryu86
217 <400> SEQUENCE: 11
218 caaagcttgg aagcaagatg gattca 26
221 <210> SEQ ID NO: 12
222 <211> LENGTH: 27
223 <212> TYPE: DNA
224 <213> ORGANISM: Artificial Sequence
226 <220> FEATURE:
227 <223> OTHER INFORMATION: HUR48

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Input Set : **A:\30215APG_SEQ.txt**
Output Set: **N:\CRF4\07272006\J508759A.raw**

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230 <400> SEQUENCE: 12
231 caagatatcc ccacaggtac cagatac                                        27
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236 <212> TYPE: DNA
237 <213> ORGANISM: Artificial Sequence
239 <220> FEATURE:
240 <223> OTHER INFORMATION: HUR49
243 <400> SEQUENCE: 13
244 tgtggggata tcttgatgac ccaaact                                         27
247 <210> SEQ ID NO: 14
248 <211> LENGTH: 27
249 <212> TYPE: DNA
250 <213> ORGANISM: Artificial Sequence
252 <220> FEATURE:
253 <223> OTHER INFORMATION: HUR50
256 <400> SEQUENCE: 14
257 cacagatctt ttgatttcca gcttggt                                         27
260 <210> SEQ ID NO: 15
261 <211> LENGTH: 27
262 <212> TYPE: DNA
263 <213> ORGANISM: Artificial Sequence
265 <220> FEATURE:
266 <223> OTHER INFORMATION: HUR51
269 <400> SEQUENCE: 15
270 atcaaaagat ctgtggctgc accatct                                         27
273 <210> SEQ ID NO: 16
274 <211> LENGTH: 58
275 <212> TYPE: DNA
276 <213> ORGANISM: Artificial Sequence
278 <220> FEATURE:
279 <223> OTHER INFORMATION: CK1D
282 <400> SEQUENCE: 16
283 gcgccgtcta gaattaacac tctcccctgt tgaagctctt tgtgacgggc gaactcag        58
286 <210> SEQ ID NO: 17
287 <211> LENGTH: 27
288 <212> TYPE: DNA
289 <213> ORGANISM: Artificial Sequence
291 <220> FEATURE:
292 <223> OTHER INFORMATION: YM001N
295 <400> SEQUENCE: 17
296 ccggaattca cattcacgat gtacttg                                         27
299 <210> SEQ ID NO: 18
300 <211> LENGTH: 16
301 <212> TYPE: DNA
302 <213> ORGANISM: Artificial Sequence
304 <220> FEATURE:
305 <223> OTHER INFORMATION: YM003
308 <400> SEQUENCE: 18
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Input Set : **A:\30215APG_SEQ.txt**
Output Set: **N:\CRF4\07272006\J508759A.raw**

309 tgcccccaga ggtgct 16
312 <210> SEQ ID NO: 19
313 <211> LENGTH: 33
314 <212> TYPE: DNA
315 <213> ORGANISM: Artificial Sequence
317 <220> FEATURE:
318 <223> OTHER INFORMATION: ym257
321 <400> SEQUENCE: 19
322 acgcattcag tgcttcttgg atgaactggg tga 33
325 <210> SEQ ID NO: 20
326 <211> LENGTH: 31
327 <212> TYPE: DNA
328 <213> ORGANISM: Artificial Sequence
330 <220> FEATURE:
331 <223> OTHER INFORMATION: YM258
334 <400> SEQUENCE: 20
335 atccaagaag cactgaatgc gtagccagaa g 31
338 <210> SEQ ID NO: 21
339 <211> LENGTH: 38
340 <212> TYPE: DNA
341 <213> ORGANISM: Artificial Sequence
343 <220> FEATURE:
344 <223> OTHER INFORMATION: YM004
347 <400> SEQUENCE: 21
348 ccaattcaaa gcggtttttc cattactata taagaggc 38
351 <210> SEQ ID NO: 22
352 <211> LENGTH: 32
353 <212> TYPE: DNA
354 <213> ORGANISM: Artificial Sequence
356 <220> FEATURE:
357 <223> OTHER INFORMATION: YM009
360 <400> SEQUENCE: 22
361 gcagccaccg tacgtttgat ttccaccttg gt 32
364 <210> SEQ ID NO: 23
365 <211> LENGTH: 39
366 <212> TYPE: DNA
367 <213> ORGANISM: Artificial Sequence
369 <220> FEATURE:
370 <223> OTHER INFORMATION: Ryu 166
373 <400> SEQUENCE: 23
374 ggatttgtct gcagtcattg tggctctgcc ctggaactt 39
377 <210> SEQ ID NO: 24
378 <211> LENGTH: 27
379 <212> TYPE: DNA
380 <213> ORGANISM: Artificial Sequence
382 <220> FEATURE:
383 <223> OTHER INFORMATION: Hur 37
386 <400> SEQUENCE: 24
387 gacaaatcca cgagcacagt ctacatg 27

Please correct similar error in subsequent sequences.

VERIFICATION SUMMARY DATE: 07/27/2006
PATENT APPLICATION: **US/10/508,759A** TIME: 09:57:34

Input Set : **A:\30215APG_SEQ.txt**
Output Set: **N:\CRF4\07272006\J508759A.raw**

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date